# Supporting Information

# Development of a sensitive, scalable method for spatial, cell-type-resolved proteomics of the human brain.

*Simon Davis*[1#], *Connor* Scott[2#], *Olaf* Ansorge[2ǂ]* *and Roman Fischer*[1ǂ]*

[1]Target Discovery Institute, Nuffield Department of Medicine, University of Oxford, Roosevelt Drive, Oxford, OX3 7FZ, UK

[2]Academic Unit of Neuropathology, Nuffield Department of Clinical Neurosciences, University of Oxford, John Radcliffe Hospital, Oxford, OX3 9DU, UK

[#, ǂ]equal contributions

*correspondence: roman.fischer@ndm.ox.ac.uk or olaf.ansorge@ndcn.ox.ac.uk

Phone: +44 1865 743639

# Table of contents

## Supplementary Figures

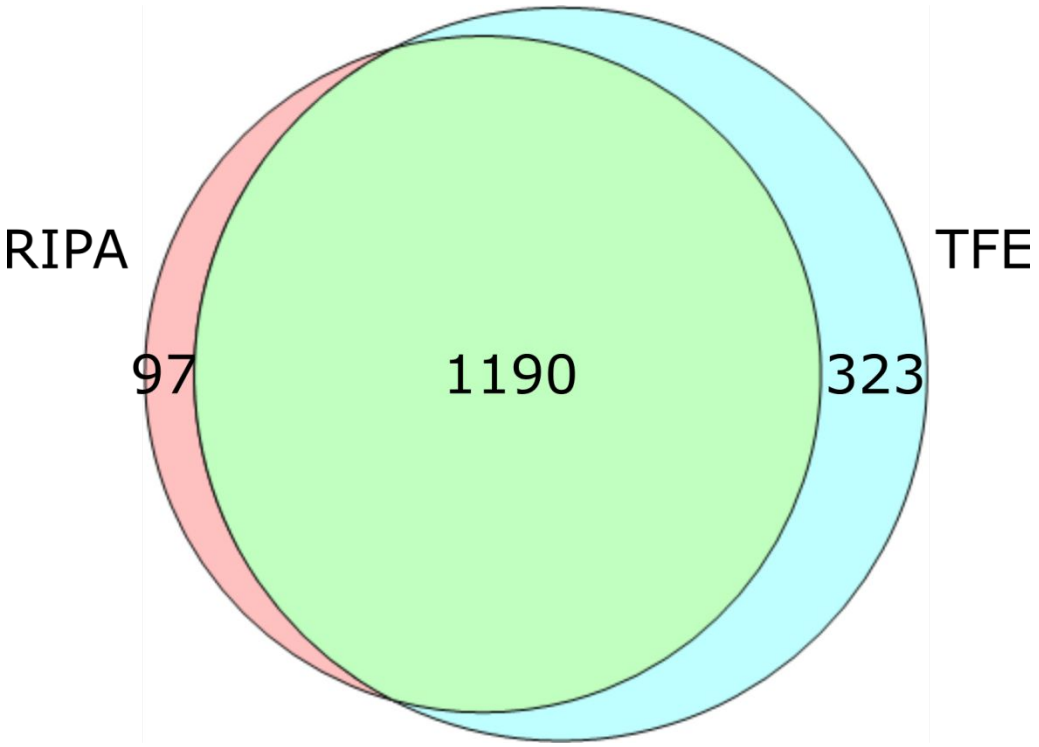


**Figure S1 – Identification overlap of proteins detected in RIPA and TFE**

The overlap in protein identifications between the two methods with the most identifications (Buffer-TFE-SP3 and Buffer-RIPA-SP3) considering proteins identified in at least two replicates per condition.

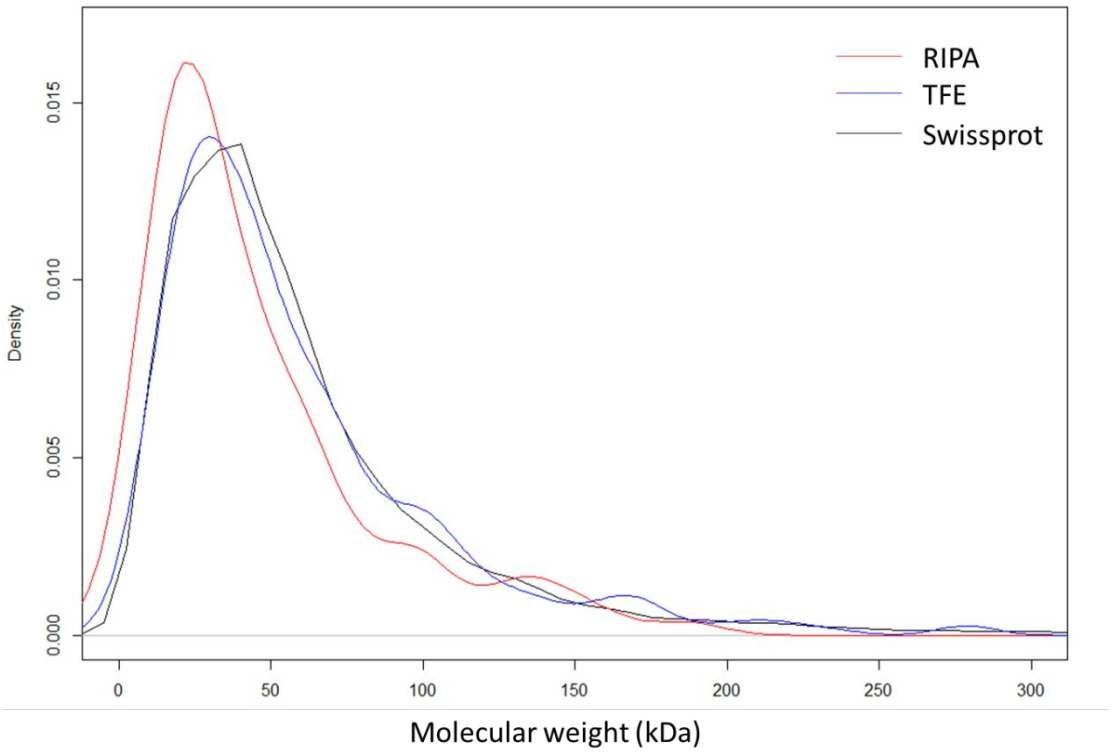


**Figure S2 – Protein molecular weight distributions**

Kernel density estimates of the distribution of the molecular weight of proteins identified in samples processed with RIPA and TFE lysis buffers compared to that of all human proteins in the SwissProt database.

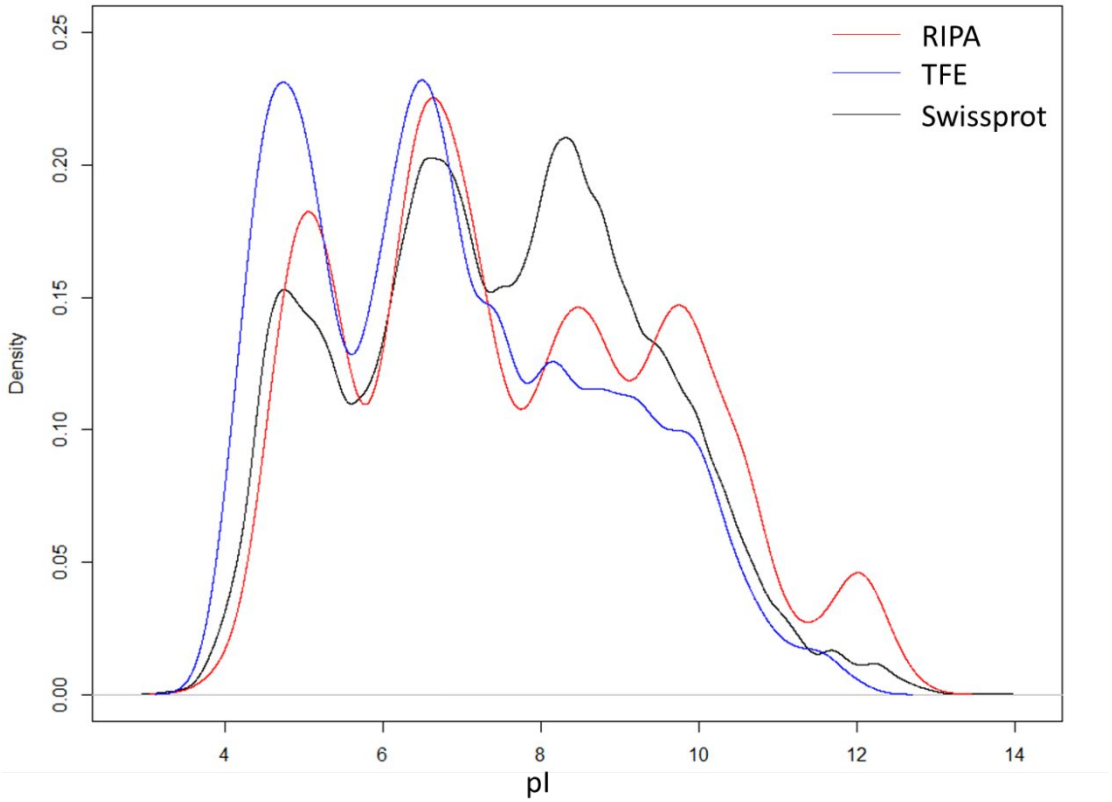


**Figure S3 – Protein isoelectric point distributions**

Kernel density estimates of the distribution of the isoelectric point of proteins identified in samples processed with RIPA and TFE lysis buffers compared to that of all human proteins in the SwissProt database.

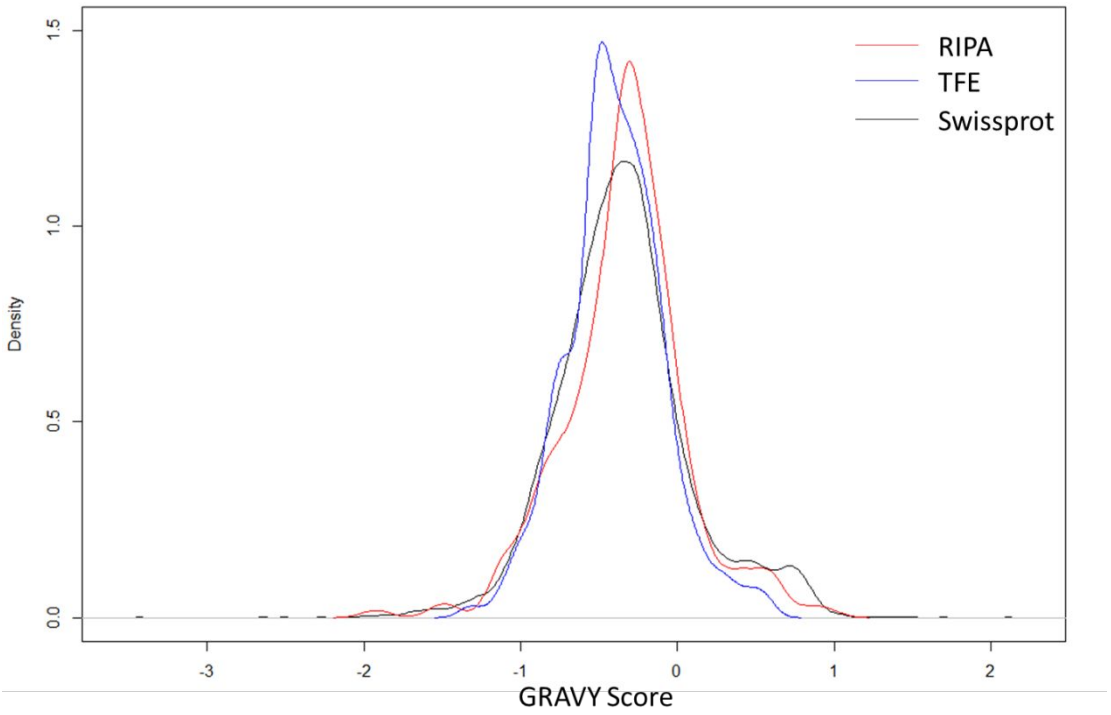


**Figure S4 – Protein GRAVY score distributions**

Kernel density estimates of the distribution of GRAVY hydropathy of proteins identified in samples processed with RIPA and TFE lysis buffers compared to that of all human proteins in the SwissProt database.

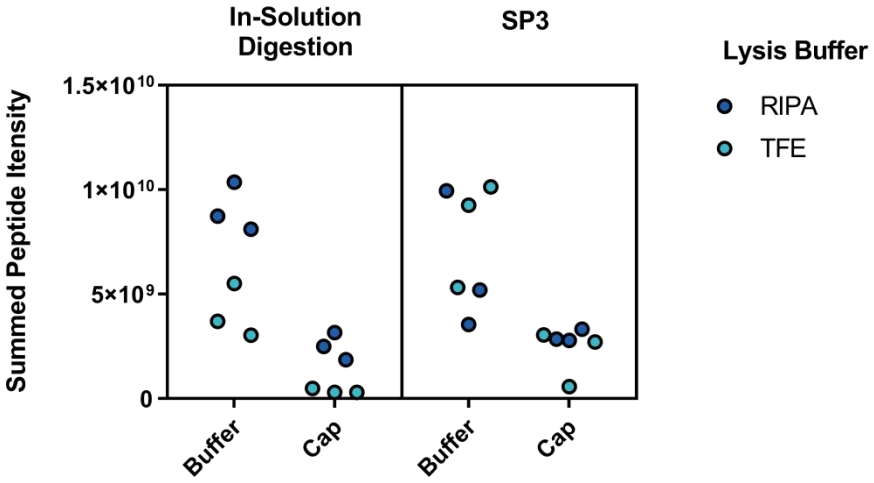


**Figure S5 – Summed peptide intensity of RIPA and TFE samples**

Summed MaxQuant peptide intensities of molecular layer optimisation experiments processed with RIPA and TFE lysis buffers using either the in-solution digestion or SP3 digestion methods after collecting into either lysis buffer or directly onto the LCM cap.

## Supporting Tables

**Table S1 – Comparison of several published LCM proteomics methods**

**Table S2 – MaxQuant protein groups output table**